REPRESENTATION, MODELING, ANALYSIS AND VISUALIZATION OF BIOLOGICAL SHAPE, FORM AND SIZE
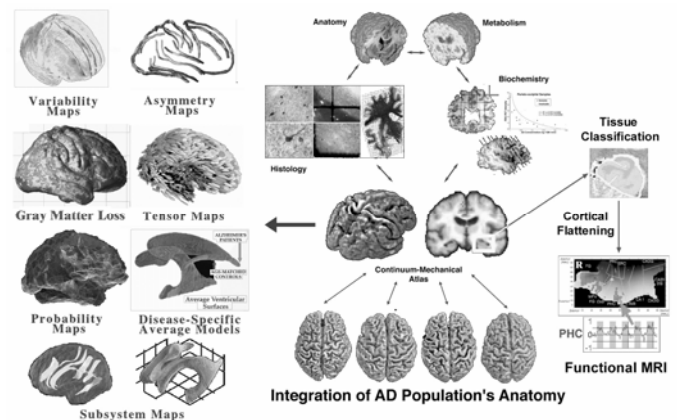
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Abstract:
The Center for Computational Biology (CCB) develops and disseminated models and computational tools to build one clearly defined and extremely important computational biology resource – a *computational brain atlas*. This computational brain atlas is an interactive environment for integrating brain anatomies, maps, alignments, shape descriptors and scientific findings. This computational framework permits large-scale, ad hoc analysis of a set of maps – each defining a view or model of scientific information. In other words, this atlas framework is a computational environment that permits researchers to collaboratively compute, combine, compare, edit, browse, and query scientific information about biological shape.

The schematic on the Figure above, relates biological shape (anatomic models, average image templates) and functional, metabolic and histologic data in a multi-modality, multi-resolution, population-specific brain atlas. This example shows registering individual volume data to a common 3D coordinate space, shape modeling (bottom), shape feature extraction (upper left), shape characterization (tissue maps) and other derived computational maps (growth, variance, or statistical maps of genetic effects) all residing in a common digital reference framework. These maps and shape models are aligned with imaging and meta-data from other modalities, using novel techniques. Shape (cortical) models from individual patients are averaged to produce an average 3D brain template for the group with well-resolved sulci in their mean locations (middle). Deviation of new individuals from the healthy control database, individual gray matter loss, asymmetry, shape complexity and other quantitative inferences can then be

The CCB *Computational Brain Atlas* Environment.

computed by aligning and comparing the subject data with the computational brain atlas (template).

Over the past two years, we have developed new mathematical formalizations for representing biological shape and advanced statistical methods for analyzing shape variation in health and disease. We also engineered new computational and visualization tools for integration of large amounts of biological data.